SEQUENCE LISTING

<110> PARANHOS-BACCALA, Glaucia
KOMURIAN-PRADEL, Florence
BEDIN, Frederic
SODOYER, Mireille
OTT, Catherine
MALLET, Francois
PERRON, Herve
MANDRAND, Bernard

<120> RETROVIRAL NUCLEIC MATERIAL AND NUCLEOTIDE FRAGMENTS, IN PARTICULAR ASSOCIATED WITH MULTIPLE SCLEROSIS AND/OR RHEUMATOID ARTHRITIS, FOR DIAGNOSTIC, PROPHYLACTIC AND THERAPEUTIC USES

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<140> US/09/319,156
<141> 1999-11-02

<150> PCT/FR98/01460
<151> 1998-07-07

<150> FR/97/08816
<151> 1997-07-07

<160> 45

<170> PatentIn version 3.2

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agccactgag gaaggaaaaa tactttcacc tgcagctaac caacagaaat tacttaaaac 180

ccttcaccaa accttccact taggcattga tagcacccat cagatggcca aattattatt 240

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Thr Phe Leu Pro Ser Arg Trp Leu Ala Thr Glu Glu Gly Lys Ile Leu
35 40 45

Ser Pro Ala Ala Asn Gln Gln Lys Leu Leu Lys Thr Leu His Gln Thr
50 55 60

Phe His Leu Gly Ile Asp Ser Thr His Gln Met Ala Lys Leu Leu Phe
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Thr Gly Pro Gly Leu Phe Lys Thr Ile Lys Lys Ile Val Arg Gly Cys
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Glu Val Cys Gln Arg Asn Asn
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Met Thr Lys Ile His Arg Gly Pro Leu Asp Arg Pro Ala Ser Pro Cys
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Ser Asp Val Asn Asp Ile Glu Gly Thr Pro Pro Glu Glu Ile Ser Thr
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Pro Tyr Gln Glu Phe Leu Xaa Arg Thr Arg Leu Pro Gly Asn Ile Asp
35 40 45

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Ala Pro Ser Tyr Arg Ser Leu Ser Lys Gly Asn Ser Thr Phe Thr Ala
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His Thr His Met Pro Arg Asn Cys Tyr Asn Ser Ala Thr Leu Cys Met
65                  70                  75                  80

His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys
                85                  90                  95

Pro Gly Gly Leu Gly Ala Thr Val Cys Trp Thr Tyr Phe Thr His Thr
            100                 105                 110

Ser Met Ser Asp Gly Gly Gly Ile Gln Gly Gln Ala Arg Glu Lys Gln
        115                 120                 125

Val Lys Glu Ala Ile Ser Gln Leu Thr Arg Gly His Ser Thr Pro Ser
    130                 135                 140

Pro Tyr Lys Gly Leu Val Leu Ser Lys Leu His Glu Thr Leu Arg Thr
145                 150                 155                 160

His Thr Arg Leu Val Ser Leu Phe Asn Thr Thr Leu Thr Arg Leu His
                165                 170                 175

Glu Val Ser Ala Gln Asn Pro Thr Asn Cys Trp Met Cys Leu Pro Leu
            180                 185                 190

His Phe Arg Pro Tyr Ile Ser Ile Pro Val Pro Glu Gln Trp Asn Asn
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Phe Ser Thr Glu Ile Asn Thr Thr Ser Val Leu Val Gly Pro Leu Val
    210                 215                 220

Ser Asn Leu Glu Ile Thr His Thr Ser Asn Leu Thr Cys Val Lys Phe
225                 230                 235                 240

Ser Asn Thr Ile Asp Thr Thr Ser Ser Gln Cys Ile Arg Trp Val Thr
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Pro Pro Thr Arg Ile Val Cys Leu Pro Ser Gly Ile Phe Phe Val Cys
            260                 265                 270

Gly Thr Ser Ala Tyr His Cys Leu Asn Gly Ser Ser Glu Ser Met Cys
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Phe Leu Ser Phe Leu Val Pro Pro Met Thr Ile Tyr Thr Glu Gln Asp
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Leu Tyr Asn His Val Val Pro Lys Pro His Asn Lys Arg Val Pro Ile
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Ile Gly Ser Ile Thr Thr Ser Thr Gln Phe Tyr Tyr Lys Leu Ser Gln
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Glu Ile Asn Gly Asp Met Glu Gln Val Thr Asp Ser Leu Val Thr Leu
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Gln Asp Gln Leu Asn Ser Leu Ala Ala Val Val Leu Gln Asn Arg Arg
    370                 375                 380

Ala Leu Asp Leu Leu Thr Ala Lys Arg Gly Gly Thr Cys Leu Phe Leu
385                 390                 395                 400

Gly Glu Glu Arg Cys Tyr Tyr Val Asn Gln Ser Arg Ile Val Thr Glu
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Lys Val Lys Glu Ile Arg Asp Arg Ile Gln Cys Arg Ala Glu Glu Leu
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Gln Asn Thr Glu Arg Trp Gly Leu Leu Ser Gln Trp Met Pro Trp Val
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Leu Pro Phe Leu Gly Pro Leu Ala Ala Leu Ile Leu Leu Leu Leu Phe
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aatttgagat cgaatataat gtagagcaga ggaccttcaa aacactgcac cctggggcct 180

cctcagccaa tggatgccct ggactctccc cttcttagga cctctagcag ctataatatt 240

tttactcctc tttggaccct gtatcttcaa cttccttgtt aagtttgtct cttccagaat 300

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aatctaccgt ggacccctgg accggcctgc tagactatgc tctgatgtta atgacattga 420

agtcacccct cccgaggaaa tctcaactgc acaaccccta ctacactcca attcagtagg 480

aagcagttag agcagttgtc agccaacctc cccaacagta cttgggtttt cctgttgaga 540

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anctgggaag gtgaccgcat ccatctttaa acatggggct tgcaacttag ctcacacccg 660

accaatcaga gagctcacta aaatgctaat caggcaaaaa caggaggtaa agcaatagcc 720

aatcatctat tgcctgagag cacagcggga aggacaagga ttgggatata aactcaggca 780

ttcaagccag caacagcaac ccccttggg tcccctccca ttgtatggga gctctgtttt 840

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35 40 45

Ala Glu Asp Leu Gln Asn Thr Ala Pro Trp Gly Leu Leu Ser Gln Trp
50 55 60

Met Pro Trp Thr Leu Pro Phe Leu Gly Pro Leu Ala Ala Ile Ile Phe
65 70 75 80

Leu Leu Leu Phe Gly Pro Cys Ile Phe Asn Phe Leu Val Lys Phe Val
85 90 95

Ser Ser Arg Ile Glu Ala Val Lys Leu Gln Ile Val Leu Gln Met Glu
100 105 110

Pro Gln Met Gln Ser Met Thr Lys Ile Tyr Arg Gly Pro Leu Asp Arg
115 120 125

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actaagaatc cataactatc ccccaaaaag caggacttag cccatacgag atgctatatg 600

gatggccttt cctaaccaat gaccttgtgc ttgactgaga aatggccaac ttagttgcag 660

acatcacctc cttagccaaa tatcaacaag ttcttaaaac atcacaggga acctgtcccc 720

gagaggaggg aaaggaacta ttccaccctg gtgacatg 758

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ggagggcaaa tggagtgaag tgccatatgt gcaaactttc ttttcattaa gagacaactc 240

acaattatgt aaaaagtgtg gtttatgccc tacaggaagc cctcagagtc cacctcccta 300

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Pro Leu Gln Gly Arg Glu Thr Trp Leu Pro Glu Gly Ser Ile Asn Tyr
35 40 45

Asn Ile Ile Leu Gln Leu Asp Leu Phe Cys Arg Lys Glu Gly Lys Trp
50 55 60

Ser Glu Val Pro Tyr Val Gln Thr Phe Phe Ser Leu Arg Asp Asn Ser
65 70 75 80

Gln Leu Cys Lys Lys Cys Gly Leu Cys Pro Thr Gly Ser Pro Gln Ser
85 90 95

Pro Pro Pro Tyr Pro Ser Val Pro Ser Pro Thr Pro Ser Ser Thr Asn
100 105 110

Lys Asp Pro Pro Leu Thr Gln Thr Val Gln Lys Glu Ile Asp Lys Gly
115 120 125

Val Asn Asn Glu Pro Lys Ser Ala Asn Ile Pro Arg Leu Cys Pro Leu
130 135 140

Gln Ala Val Arg Gly Gly Glu Phe Gly Pro Ala Arg Val Pro Val Pro
145 150 155 160

Phe Ser Leu Ser Asp Leu Lys Gln Ile Lys Ile Asp Leu Gly Lys Phe
165 170 175

Ser Asp Asn Pro Asp Gly Tyr Ile Asp Val Leu Gln Gly Leu Gly Gln
180 185 190

Ser Phe Asp Leu Thr Trp Arg Asp Ile Met Leu Leu Leu Asn Gln Thr
195 200 205

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Gly Asp Leu Trp Tyr Leu Ser Gln Ala Asn Asn Arg Met Thr Thr Glu
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Glu Arg Thr Thr Pro Thr Gly Gln Gln Ala Val Pro Ser Val Asp Pro
                245                 250                 255

His Trp Asp Thr Glu Ser Glu His Gly Asp Trp Cys His Lys His Leu
            260                 265                 270

Leu Thr Cys Val Leu Glu Gly Leu Arg Lys Thr Arg Lys Lys Pro Met
        275                 280                 285

Asn Tyr Ser Met Met Ser Thr Ile Thr Gln Gly Lys Glu Glu Asn Leu
    290                 295                 300

Thr Ala Phe Leu Asp Arg Leu Arg Glu Ala Leu Arg Lys His Thr Ser
305                 310                 315                 320

Leu Ser Pro Asp Ser Ile Glu Gly Gln Leu Ile Leu Lys Asp Lys Phe
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        35                  40                  45

Leu Arg Lys Lys Arg Phe Ile Phe Phe Cys Ser Thr Ala Trp Pro Gln
    50                  55                  60

Tyr Pro Leu Gln Gly Arg Glu Thr Trp Leu Pro Glu Gly Ser Ile Asn
65                  70                  75                  80

Tyr Asn Ile Ile Leu Gln Leu Asp Leu Phe Cys Arg Lys Glu Gly Lys
                85                  90                  95

Trp Ser Glu Val Pro Tyr Val Gln Thr Phe Phe Ser Leu Arg Asp Asn
            100                 105                 110

Ser Gln Leu Cys Lys Lys Cys Gly Leu Cys Pro Thr Gly Ser Pro Gln
        115                 120                 125

Ser Pro Pro Pro Tyr Pro Ser Val Pro Ser Pro Thr Pro Ser Ser Thr
    130                 135                 140

Asn Lys Asp Pro Pro Leu Thr Gln Thr Val Gln Lys Glu Ile Asp Lys
145                 150                 155                 160

Gly Val Asn Asn Glu Pro Lys Ser Ala Asn Ile Pro Arg Leu Cys Pro
                165                 170                 175

Leu Gln Ala Val Arg Gly Gly Glu Phe Gly Pro Ala Arg Val Pro Val
            180                 185                 190

Pro Phe Ser Leu Ser Asp Leu Lys Gln Ile Lys Ile Asp Leu Gly Lys
        195                 200                 205

Phe Ser Asp Asn Pro Asp Gly Tyr Ile Asp Val Leu Gln Gly Leu Gly
    210                 215                 220

Gln Ser Phe Asp Leu Thr Trp Arg Asp Ile Met Leu Leu Leu Asn Gln
225                 230                 235                 240

Thr Leu Thr Pro Asn Glu Arg Ser Ala Ala Val Thr Ala Ala Arg Glu
                245                 250                 255

Phe Gly Asp Leu Trp Tyr Leu Ser Gln Ala Asn Asn Arg Met Thr Thr
            260                 265                 270

Glu Glu Arg Thr Thr Pro Thr Gly Gln Gln Ala Val Pro Ser Val Asp
        275                 280                 285
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Pro His Trp Asp Thr Glu Ser Glu His Gly Asp Trp Cys His Lys His
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Leu Leu Thr Cys Val Leu Glu Gly Leu Arg Lys Thr Arg Lys Lys Pro
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325 330 335

Leu Thr Ala Phe Leu Asp Arg Leu Arg Glu Ala Leu Arg Lys His Thr
340 345 350

Ser Leu Ser Pro Asp Ser Ile Glu Gly Gln Leu Ile Leu Lys Asp Lys
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Gly Arg Glu Thr Trp Leu Pro Glu Gly Ser Ile Asn Tyr Asn Ile Ile
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Leu Gln Leu Asp Leu Phe Cys Arg Lys Glu Gly Lys Trp Ser Glu Val
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Pro Tyr Val Gln Thr Phe Phe Ser Leu Arg Asp Asn Ser Gln Leu Cys
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Lys Lys Cys Gly Leu Cys Pro Thr Gly Ser Pro Gln Ser Pro Pro Pro
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Tyr Pro Ser Val Pro Ser Pro Thr Pro Ser Ser Thr Asn Lys Asp Pro
115 120 125

Pro Leu Thr Gln Thr Val Gln Lys Glu Ile Asp Lys Gly Val Asn Asn
130 135 140

Glu Pro Lys Ser Ala Asn Ile Pro Arg Leu Cys Pro Leu Gln Ala Val
145 150 155 160

Arg Gly Gly Glu Phe Gly Pro Ala Arg Val Pro Val Pro Phe Ser Leu
165 170 175

Ser Asp Leu Lys Gln Ile Lys Ile Asp Leu Gly Lys Phe Ser Asp Asn
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Pro Asp Gly Tyr Ile Asp Val Leu Gln Gly Leu Gly Gln Ser Phe Asp
195 200 205

Leu Thr Trp Arg Asp Ile Met Leu Leu Leu Asn Gln Thr Leu Thr Pro
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Asn Glu Arg Ser Ala Ala Val Thr Ala Ala Arg Glu Phe Gly Asp Leu
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Trp Tyr Leu Ser Gln Ala Asn Asn Arg Met Thr Thr Glu Glu Arg Thr
245 250 255

Thr Pro Thr Gly Gln Gln Ala Val Pro Ser Val Asp Pro His Trp Asp
260 265 270

Thr Glu Ser Glu His Gly Asp Trp Cys His Lys His Leu Leu Thr Cys
275 280 285

Val Leu Glu Gly Leu Arg Lys Thr Arg Lys Lys Pro Met Asn Tyr Ser
290 295 300

Met Met Ser Thr Ile Thr Gln Gly Lys Glu Glu Asn Leu Thr Ala Phe
305 310 315 320

Leu Asp Arg Leu Arg Glu Ala Leu Arg Lys His Thr Ser Leu Ser Pro
325 330 335

Asp Ser Ile Glu Gly Gln Leu Ile Leu Lys Asp Lys Phe Ile Thr Gln
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tgaatccgca accatgaagg gatctccaaa gcaattggaa atgttcctcc caaggcaaaa 420

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Pro Pro Leu Ser Trp Glu Leu Trp Glu Gln Gly Pro Gln Val Thr Ile
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Trp
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ccatatgtgc aaactttctt ttcattaaga gacaactcac aattatgtaa aaagtgtggt 300

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